



Projecting PamChip® data on CORAL Kinome Tree: Inferring Group differences on phylogenetic tree

Peptides on PamChip (PTK 86402, 86412 and STK 87102) can be phosphorylated by a number of kinases. The Upstream Kinase Tool is a functional scoring method that ranks the Top kinases. Visualization of the data on a phylogenetic tree can be useful.

Kinase Score Tables from PamChip Data (Upstream Kinase Analysis PamApp Tool)

From the BioNavigator Upstream Kinase Tool, a Table of the Kinase scores and stats is generated for each comparison; Data extracted from this Table are used to plot Coral Kinome map.

Columns to use for Kinome tree

Combine the trees from the PTK and STK assay, or use them separately, using excel/ notepad. There are several Column headers in the Kinase Score Table, of which the ones listed below will be used. A thresh hold cut-off is generally defined at 1.2 of the Median Final Score, however the value depends on sample numbers (N) and specificity scores. You can also take the Top 10 from the list.

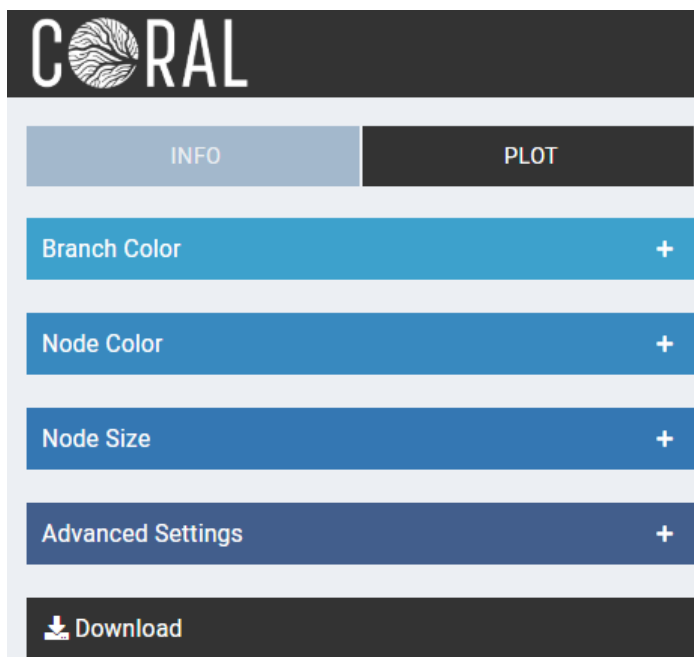
Column header	Description
Kinase UniPROT ID	Required for pathway analysis etc.
<i>Kinase Name</i>	<i>As derived from Databases (Informative only)</i>
Median Final score	Used for Scoring/ Ranking/ Ordering the Kinases
Median Kinase Statistic	Used for Effect size and direction (<0= inhibition; >0 =stimulation; compared in Control/ baseline)

Mapping using Web-based Tool

Use the URL: <http://phanstiel-lab.med.unc.edu/CORAL/>. Go to the PLOT Tab.

Configuring the Kinome tree with PamChip data

Each sub section under the PLOT Tab can be independently configured. You can choose how to colour the tree. Use the pull down menus, and select quantitative settings to configure.





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Configuring the Kinome tree with PamChip data

Each sub-section under the PLOT Tab can be independently configured. You can choose how to colour the tree. Use the pull down menus, and select quantitative settings to configure color scheme and labels.

Copy-paste the 2 relevant columns as described below from the Score Table. Choose identifier UniPROT.

NODE COLOR: UniPROT ID and Median Kinase Statistic. This provides the effect size and direction. You can choose colors, scales and rename the labels.

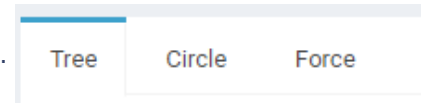
NODE SIZE: UniPROT ID and Median Final Score. Size provides the Rank order of the Kinases. You can choose colors, scales and rename the labels.

BRANCH colour can be optionally set by uploading list or manually using vales as for node colour described above

ADVANCED SETTINGS: Add Titles. For Labels, use the Manual setting and copy-paste the UniPROT ID Only, and select identifier uniprot.

DOWNLOAD: After the tree image is created you can download the image as hi-res SVG.

You can switch to Circle or Force views as well.



Node Color

Color Scheme
Quantitative

load example data

Kinases & Value

Identifier
uniprot

Legend Subtitle

Min Value **Max Value**

Palette Type
 sequential
 divergent

label

Node Size

Scaling Scheme
Quantitative

load example data

Kinases & Value

Identifier
uniprot

Legend Subtitle

Size Range

Missing Kinases
 show
 hide
 manually set data range

Min Value **Max Value**

Advanced Settings

Title Labels Node

Label Identifier
Default

Font
Helvetica

Label Color Scheme
Manual

Kinases

Identifier
uniprot

Default Color **Selection Color**

Default Size **Selection Size**

Group Color

